

## FIG. 1A

1 ATGGAGTCGGGGCTGCTGCGGCCGGCGCCGGTGAGCGAGGTCATCGTCCTGCATTACAAC  
M E S G L L R P A P V S E V I V L H Y N

61 TACACCGGCAAGCTCCGCGGTGCGCGCTACCAGCCGGGTGCCGGCCTGCGCGCCGACGCC  
Y T G K L R G A R Y Q P G A G L R A D A

121 GTGGTGTGCCTGGCGGTGTGCGCCTTCATCGTGCTAGAGAATCTAGCCGTGTTGTTGGTG  
V V C L A V C A F I V L E N L A V L L V

181 CTCGGACGCCACCCGCGCTTCCACGCTCCCATGTTCTGCTCCTGGGCAGCCTCACGTTG  
L G R H P R F H A P M F L L L G S L T L

241 TCGGATCTGCTGGCAGGCGCCGCCTACGCCGCAACATCCTACTGTCGGGGCCGCTCACG  
S D L L A G A A Y A A N I L L S G P L T

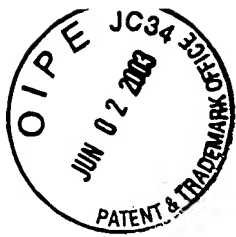
301 CTGAAACTGTCCCCCGCGCTCTGGTTCGCACGGGAGGGAGGCGTCTTCGTGGCACTCACT  
L K L S P A L W F A R E G G V F V A L T

361 GCGTCCGTGCTGAGCCTCCTGGCCATCGCGCTGGAGCGCAGCCTCACCATGGCGCGCAGG  
A S V L S L L A I A L E R S L T M A R R

421 GGGCCCCGCGCCCGTCTCCAGTCGGGGGCGCACGCTGGCGATGGCAGCCGCGGCCTGGGGC  
G P A P V S S R G R T L A M A A A A W G

481 GTGTCGCTGCTCCTCGGGCTCCTGCCAGCGCTGGGCTGGAATTGCCTGGGTGCGCTGGAC  
V S L L L G L L P A L G W N C L G R L D

541 GCTTGCTCCACTGTCTTGCCGCTCTACGCCAAGGCCTACGTGCTCTTCTGCGTGCTCGCC  
A C S T V L P L Y A K A Y V L F C V L A



## FIG. 1B

601 TTCGTGGGCATCCTGGCCGCTATCTGTGCACTCTACGCGCGCATCTACTGCCAGGTACGC  
F V G I L A A I C A L Y A R I Y C Q V R

661 GCCAACGCGCGGCGCCTGCCGGCACGGCCCCGGGACTGCGGGGACCACCTCGACCCGGGCG  
A N A R R L P A R P G T A G T T S T R A

721 CGTCGCAAGCCGCGCTCGCTGGCCTTGCTGCGCACGCTCAGCGTGGTGCTCCTGGCCTTT  
R R K P R S L A L L R T L S V V L L A F

781 GTGGCATGTTGGGGCCCCCTCTTCCTGCTGCTGTTGCTCGACGTGGCGTGCCCGGCGCGC  
V A C W G P L F L L L L L D V A C P A R

841 ACCTGTCCTGTACTCCTGCAGGCCGATCCCTTCCTGGGACTGGCCATGGCCAACTCACTT  
T C P V L L Q A D P F L G L A M A N S L

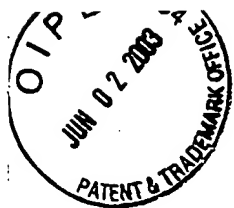
901 CTGAACCCCATCATCTACACGCTCACCAACCGCGACCTGCGCCACGCGCTCCTGCGCCTG  
L N P I I Y T L T N R D L R H A L L R L

961 GTCTGCTGCGGACGCCACTCCTGCGGCAGAGACCCGAGTGGCTCCCAGCAGTCGGCGAGC  
V C C G R H S C G R D P S G S Q Q S A S

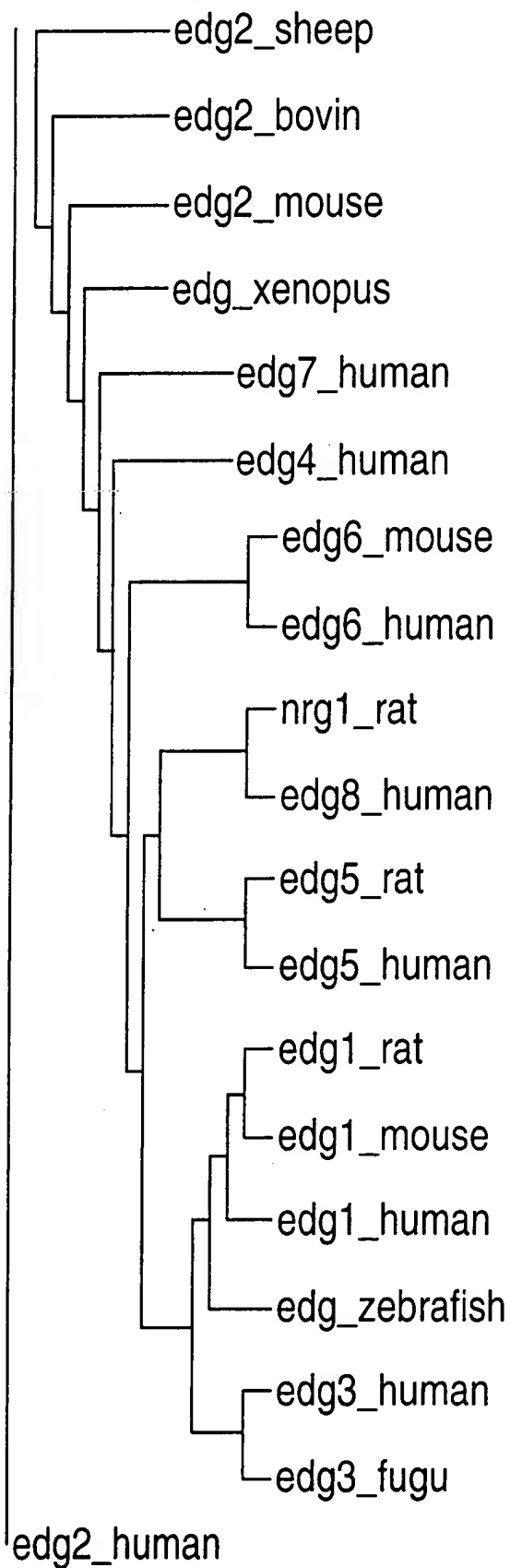
1021 GCGGCTGAGGCTTCCGGGGGCCTGCGCCGCTGCCTGCCCCCGGCCTTGATGGGAGCTTC  
A A E A S G G L R R C L P P G L D G S F

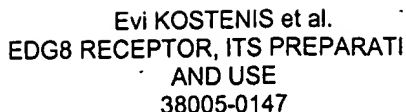
1081 AGCGGCTCGGAGCGCTCATCGCCCCAGCGCGACGGGCTGGACACCAGCGGCTCCACAGGC  
S G S E R S S P Q R D G L D T S G S T G

1141 AGCCCCGGTGACCCACAGCCGCCCGGACTCTGGTATCAGAACCGGCTGCAGACTGA  
S P G A P T A A R T L V S E P A A D \*

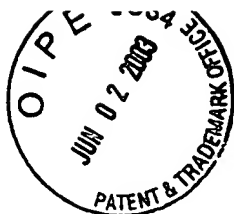


**FIG. 2**



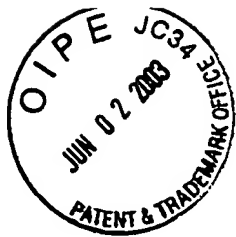


1	60
edg2_human	MAAISTSIPV ISQPQETAMN EPQCFYNESI AFFYNRSGKH LAT.EWNTVS KLVVGL..GI
edg7_human	-----MN E..CHYDKHM DFFYNRSNTD TVD.DW.TGT KLVIVLCVGT
edg4_human	-----MVI MGQCYYNETI GFFYNNSGKE LSS.HWR..P KDVVVVALGL
edg1_human	----MGPTS VPLVKAHRSS VSDYVNYDII VRHYNVTGKL ..NISADKEN SIKILTSVVF
edg3_human	-----MATALPPR LQPVRGNETL REHYQYVGKL AGRLKEASEG S.TLTTVLFL
edg5_human	-----MGSL YSEYLNPNKV QEHYNYTKE. ..TLETQETT SRQVASAFIV
edg8_human	-----MESGL LRPAPVSEVI VLHYNVTGKL RG.ARYQPGA GLRADAVVCL
edg6_human	----MNATG TPVAPESCQQ LAAGGHSRLI VLHYNHSGRL AGR.GGPEDG GLGALRGLSV
61	120
edg2_human	TVCIFIMLAN LLVMVAIYVN RRFHEPIYYL MANLAAADFF AGLAYFYLMF MTGPNTRRLT
edg7_human	FFCLFIFFSN SLVIAAVIKN RKFHFPFYLL LANLAAADFF AGIAYVFLMF NTGVPVSKTLT
edg4_human	TVSVLVLLTN LLVIAAIASN RRFHQPIYYL LGNLAAADLF AGVAYFLMF HTGPRTARLS
edg1_human	LICCFIILEN IFVLLTIWKT KKFHPMPYFF IGNLALSDLL AGVAYTANLL LSGATTYKLT
edg3_human	VICSFIVLEN LMLVIAIWN NKFHNRMYFF IGNLALCDLL AGIAYKVNL MSGKKTFSLS
edg5_human	ILCCAIVVEN LLVLIAVARN SKFHSAMYLF LGNLAASDLL AGVAFVANTL LSGSVTLRLT
edg8_human	AVCAFIVLEN LAVLLVLGRH PRFHAPMFL LGSLTSLDLL AGAAYAANIL LSGPLTLKLS
edg6_human	AASCLVVLEN LLVLAAITSH MRSRRWVYYC LVNITSLDLL TGAAYLANVL LSGARTFRLA
121	180
edg2_human	VSTWLLRQGL IDTSLTASVA NLLAIAIERH ITVFR.MQLH TRMSNRRVVV VIVVIWTMAI
edg7_human	VNRWFLRQGL LDSSLTASLT NLLVIAVERH MSIMR.MRVH SNLTKKRNTL LILLVWAIAI
edg4_human	LEGWFLRQGL LDTSLTASVA TLLAIAVERH RSVMA.VQLH SRLPRGRVVM LIVGVWVAAI
edg1_human	PAQWFLREGS MFVALSASF SLLAIAIERY ITMLK.MKLH NGSNNFRLFL LISACWVISL
edg3_human	PTVWFLREGS MFVALGASTC SLLAIAIERH LTMIK.MRPY DANKRHRVFL LIGMCWLIAF
edg5_human	PVQWFAREGS ASITLSASF SLLAIAIERH VAIK.VKLY GSDKSCRMLL LIGASWLISL
edg8_human	PALWFAREGG VFVALTASVL SLLAIAIERS LTMAR.RGPA PVSSRGRITLA MAAAAGVSL
edg6_human	PAQWFLREGL LFTALAASTF SLLFTAGERF ATMVRPVAES GATKTSPVYG FIGLCWLLAA
181	240
edg2_human	VMGAIPSVGW NCICDIENCS NMAPLYSDSY LVFWAIFNLV TFVVMVVLVA HIFGYVRQRT
edg7_human	FMGAVPTLGW NCLCNISACS SLAPIYSRSY LVFWTVSNLM AFLIMVVVYL RIYVYVVRKT
edg4_human	GLGLLPAHSW HCLCALDRCS RMAPLLRSY LAVWALSSLL VFLLMVAVYT RIFFYVRRRV
edg1_human	ILGGLPIMGW NCISALSSCS TVLPLYHKHY ILFCTTVFTL LLLSIVILYC RIYSLVRTRS
edg3_human	TLGALPILGW NCLHNLPCDS TILPLYSKKY IAFCSIFTA ILVTIVILYA RIYFLVKSSS
edg5_human	VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI ILLAIVALYV RIYCVVRSSH
edg8_human	LLGLLPALGW NCLGRLDACS TVLPLYAKAY VLFCVLAFIG ILLAICALYA RIYQVVRANA
edg6_human	LLGMLPLLGW NCLCAFDRCS SLLPLYSKRY ILFCLVIFAG VLATIMGLYG AIFRLVQASG

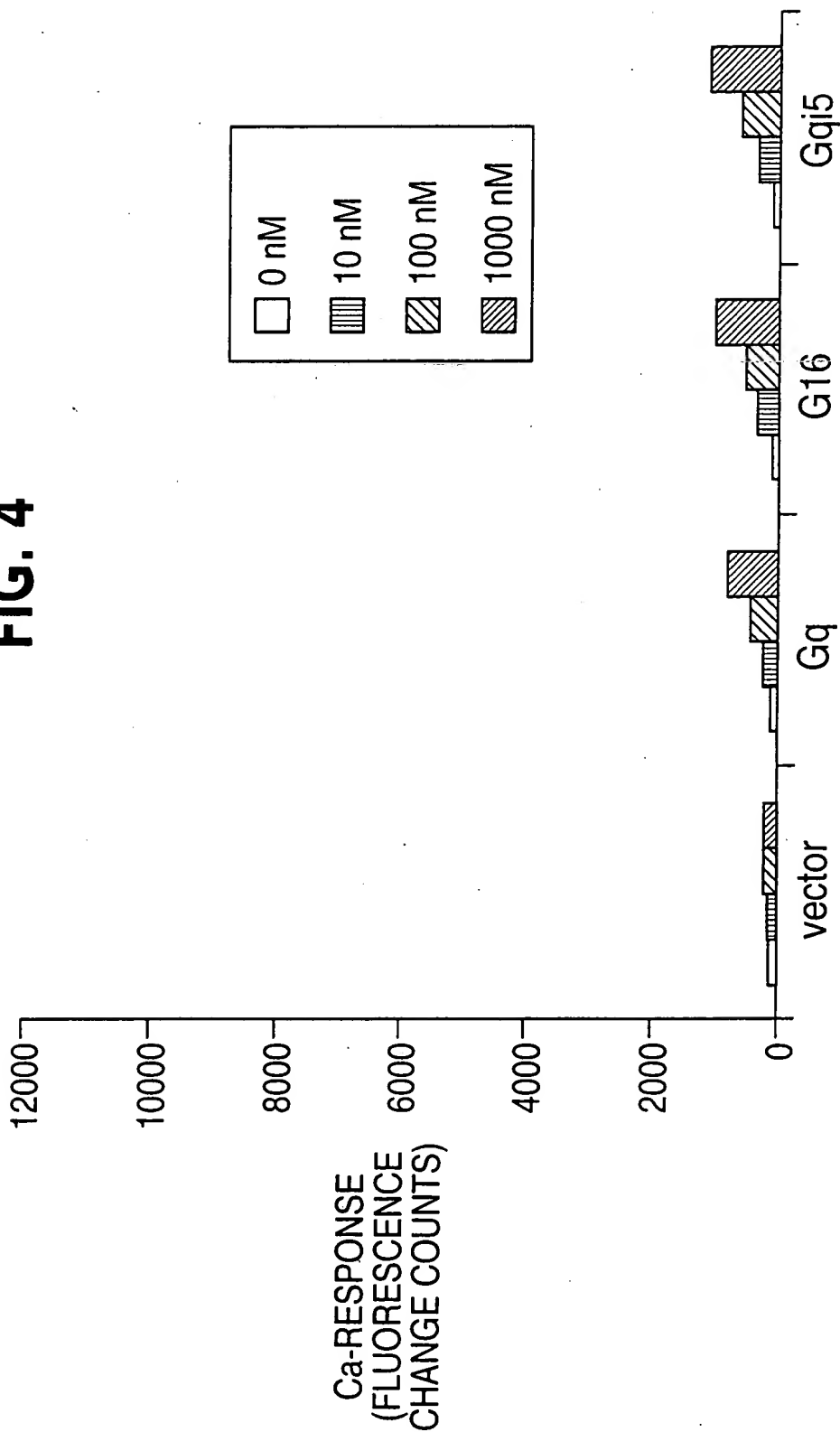


## FIG. 3B

	241		300
edg2_human	MRMSRHSSGP R.....RNR DTMSLLKTV	VIVLGAFIIC WTPGLVLLLL	D.VCCP..QC
edg7_human	NVLSPHTSGS I.....SRR RTPMKLMKTV	MTVLGAFVVC WTPGLVVLLL	DGLNCR..QC
edg4_human	QRMAEHVSCH P.....RYR ETTLSLVKTV	VIILGAFVVC WTPGQVVLLL	DGLGCE..SC
edg1_human	RRLTFR.... .KNISKASRS SENVALLKTV	IIVLSVFIAC WAPLFILLLL	DV.GCKVKTC
edg3_human	RKVANH.... .NN.....S ERSMAALLRTV	VIVVSVFIAC WSPLFILFLI	DV.ACRVQAC
edg5_human	ADMA..... .A POTLALLKTV	TIVLGVFIVC WLPAFSILL	DY.ACPVHSC
edg8_human	RRLPARPGTA GTTSTRARRK PRSLALLRTL	SVVLLAFVAC WGPLFLLLLL	DV.ACPARTC
edg6_human	QKAP..... .RPAARRK ARR..LLKTV	LMILLAFLVC WGPLFGLLLA	DVFGSNLWAO
	301		360
edg2_human	DVLAYEKFFL LLAEFNSAMN PIIYSYRDK	MSATFRQILC CQRSENPTGP	TESSDRSASS
edg7_human	GVQHVKRWFL LLALLNSVFN PIIYSYKDED	MYGTMKKMIC CFSQENP...	....ERRPSR
edg4_human	NVLAVEKYFL LLAEANSLVN AAVYSCRDAE	MRRTFRLLC CACLRSTRE	SVHYTSSAQG
edg1_human	DILFRAEYFL VLAVLNSGTN PIIYTLTNKE	MRRAFIRIMS CCKCPSGD..	.....S
edg3_human	PILFKAQWFI VLAVLNSAMN PVIYTLASKE	MRRAFFRLV. .CNC.LVR..	.....G
edg5_human	PILYKAHYFF AVSTLNSLLN PVIYTWRSRD	LRREVLRLPLQ CWRPGVGV..	.....Q
edg8_human	PVLLQADPFL GLAMANSLLN PIIYTLTNRD	LRHALLRLVC CGRHSCGRDP	SGS..QQSAS
edg6_human	EYLRGMDWIL ALAVLNSAVN PIIYSFRSRE	VCRAVLSFLC CGCLRLGMRG	PGDCLARAVE
	361		418
edg2_human	LNHTILAGVH SNDHSVV---	-----	-----
edg7_human	IPSTVLSRSD TGSQYIEDSI SQGAVCNKST	S-----	-----
edg4_human	GASTRIMLPE NGHPLMTPPF SYLELQRYAA	SNKSTAPDDL WVLLAQPNQQ	D-----
edg1_human	AGKFKRPIIA GMEFSRSK.. .SDNSSHPQK	DEGDNPETIM SSGNVNSSS-	-----
edg3_human	RGARASPIQP ALDPSRSKSS SSNNSSHSPK	VKEDLPHTDP SSCIMDKNAA	LQNGIFCN
edg5_human	GRRRVGTPGH HLLPLRSSSS LERGMHPTS	PTFLEGNTVV -----	-----
edg8_human	AAEASGGLRR CLPPGLDGSF SGSERSSPQR	DGLDTSGSTG SPGAPTAART	LVSEPAAD
edg6_human	AHSGASTTDS SLRP.RDSFR GSRSLSFRMR	EPLSSISSVR SI-----	-----



**FIG. 4**





**FIG. 5**

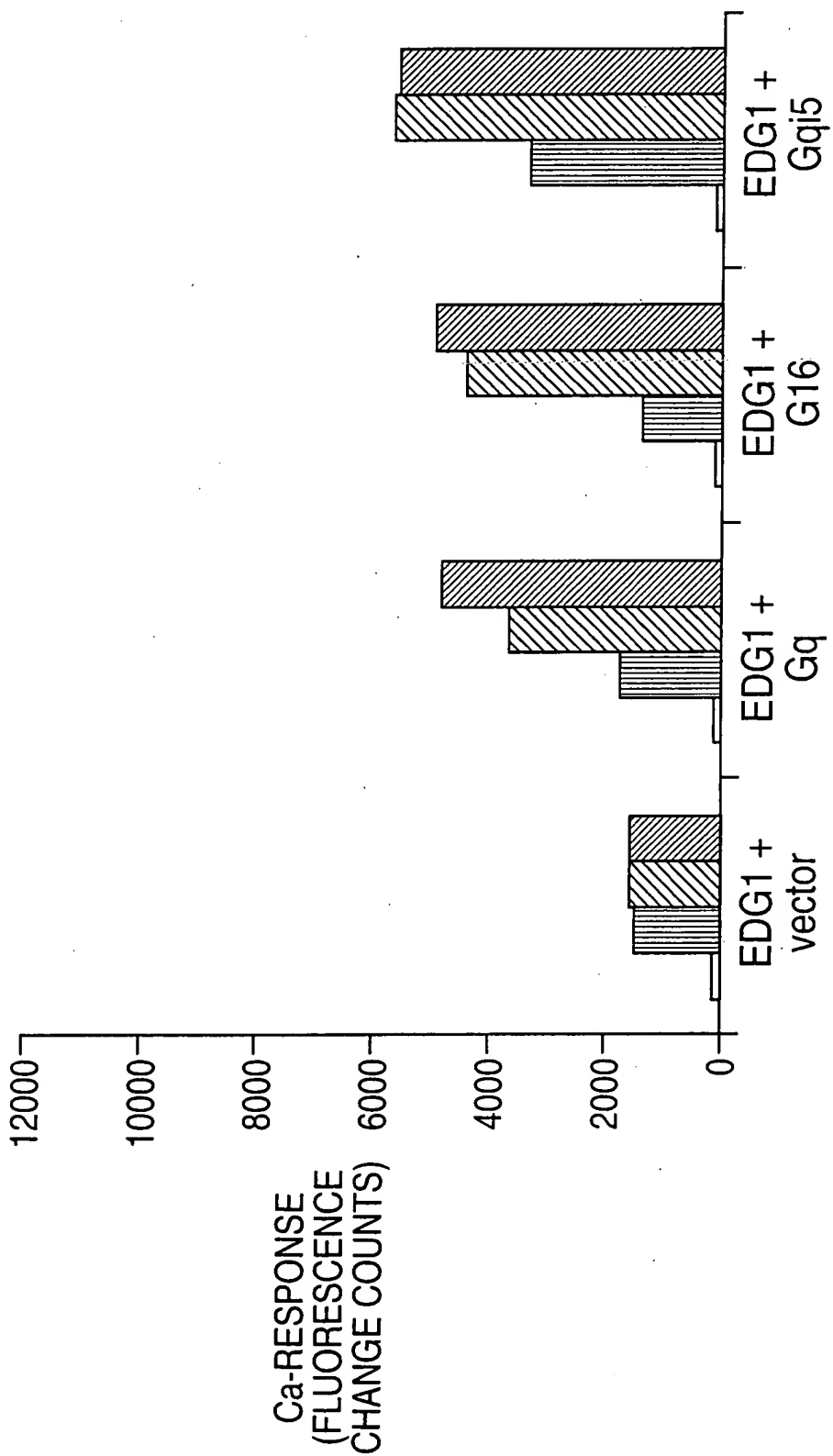




FIG. 6

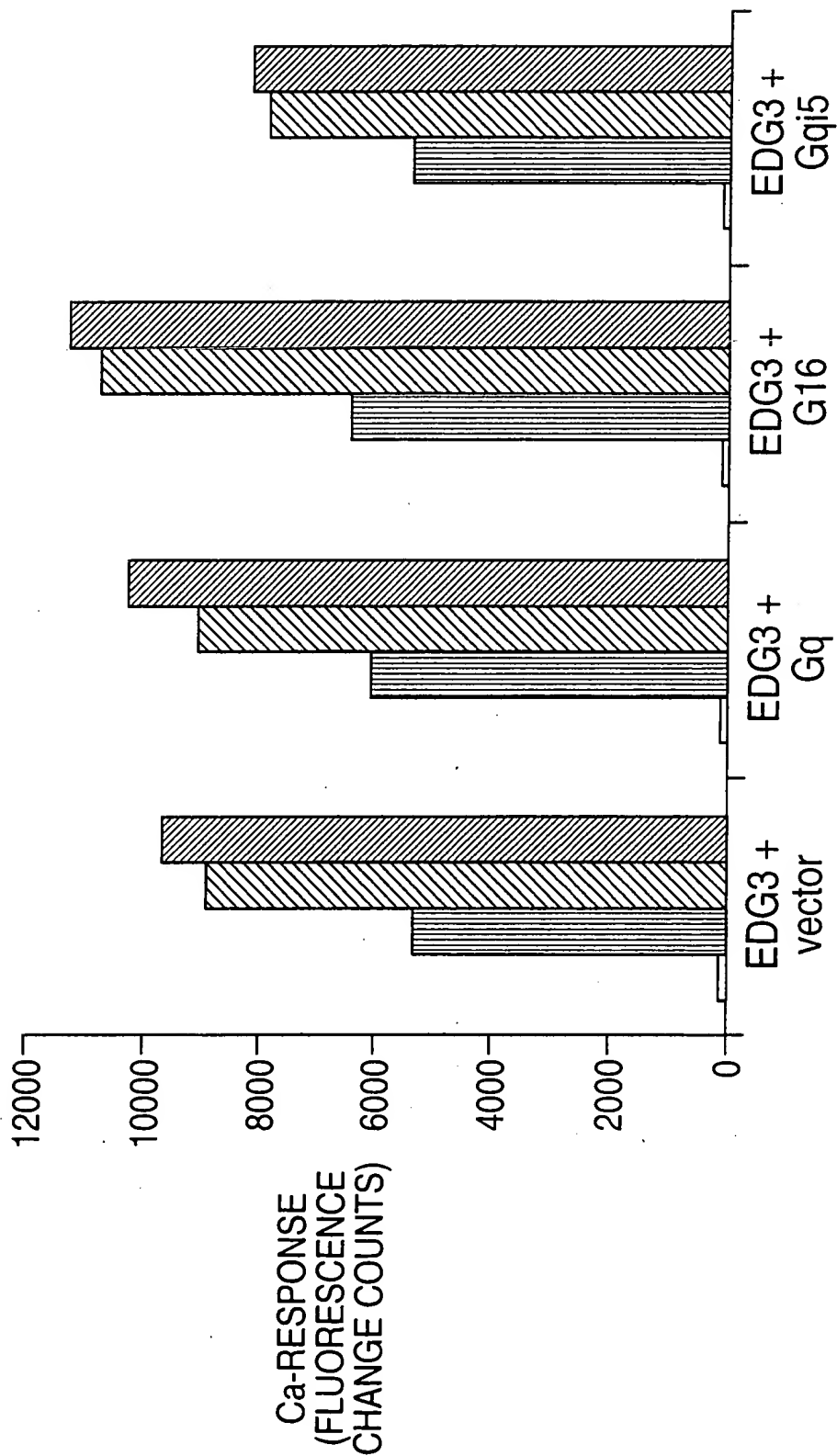
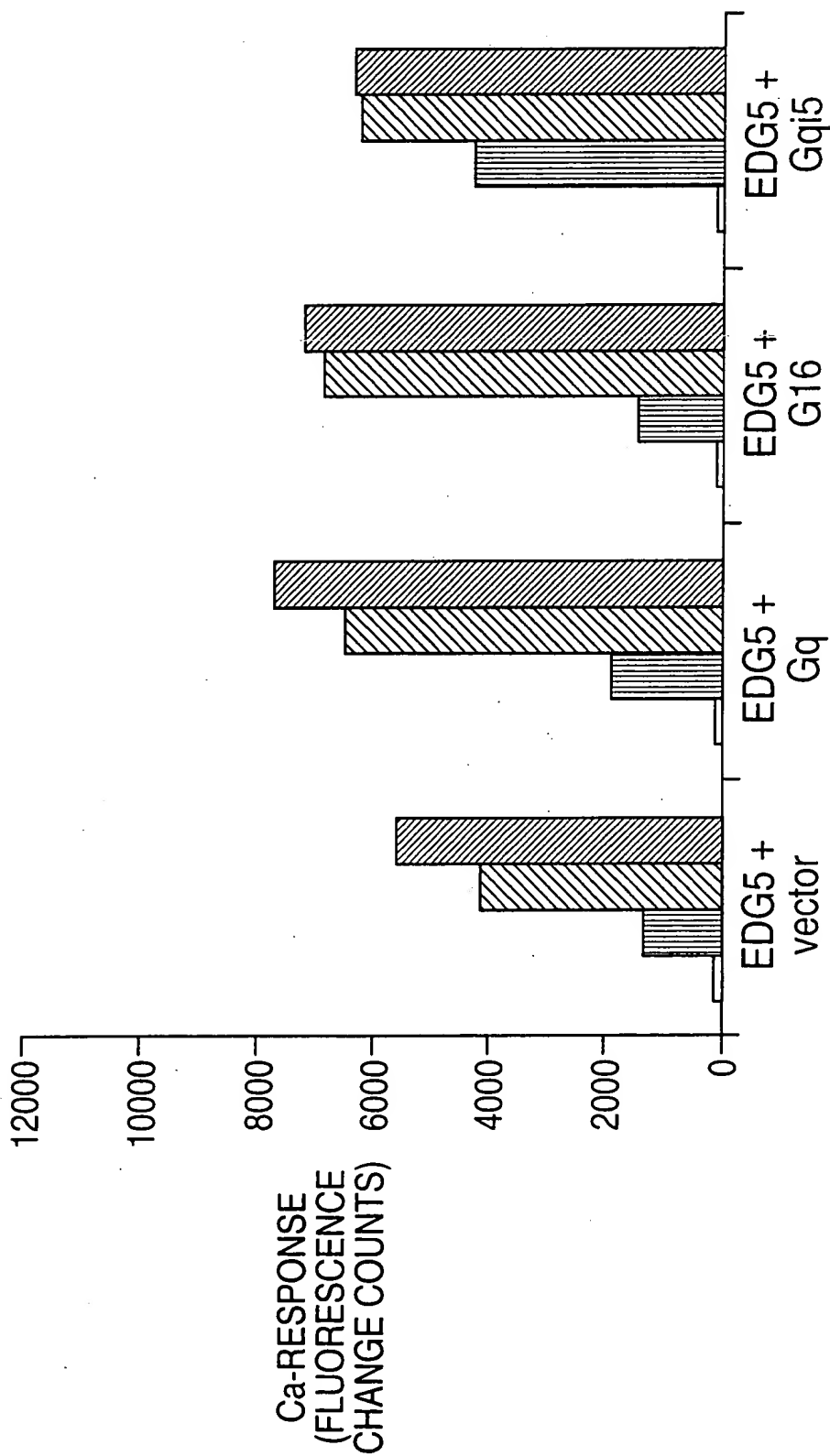


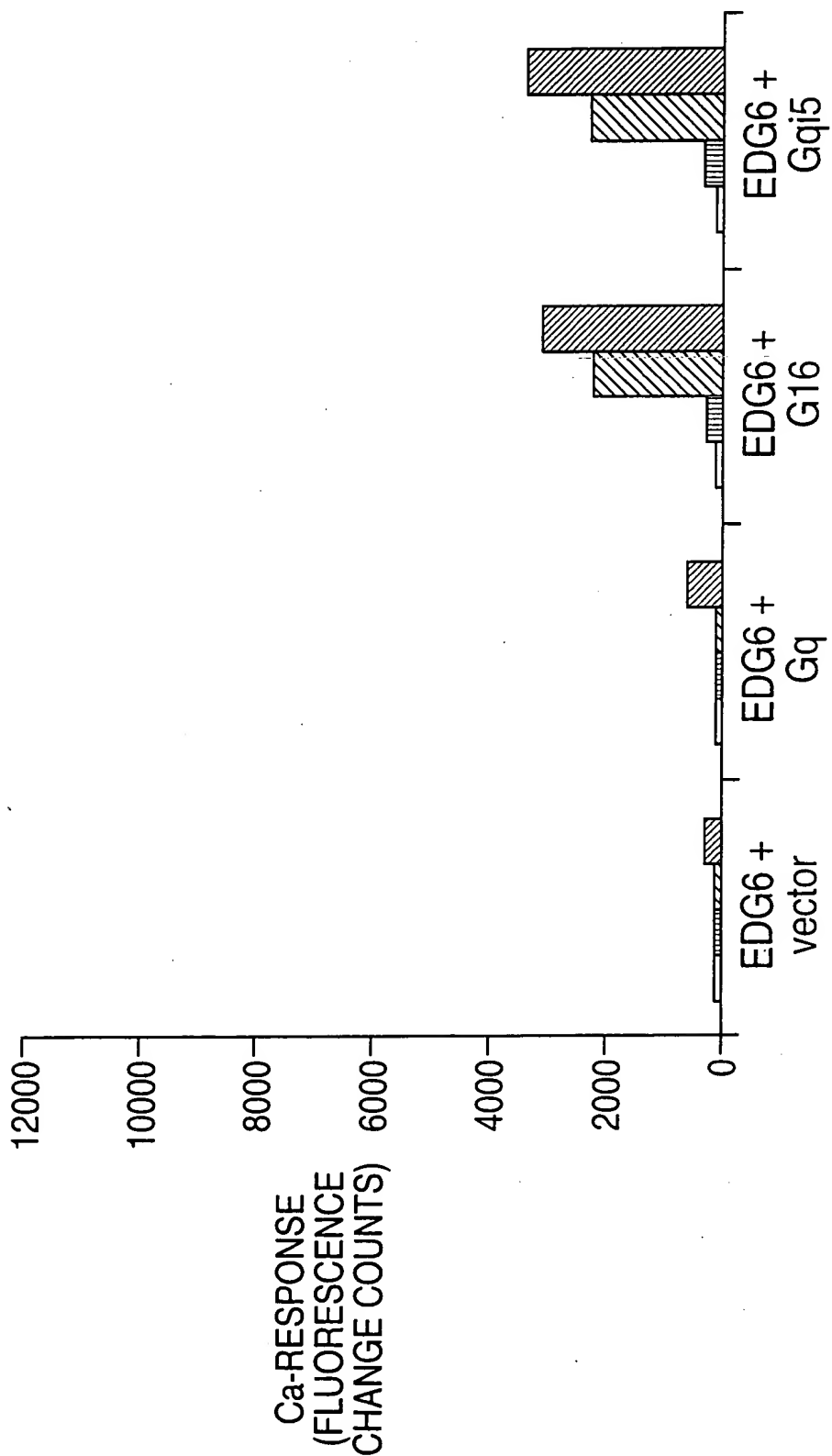


FIG. 7



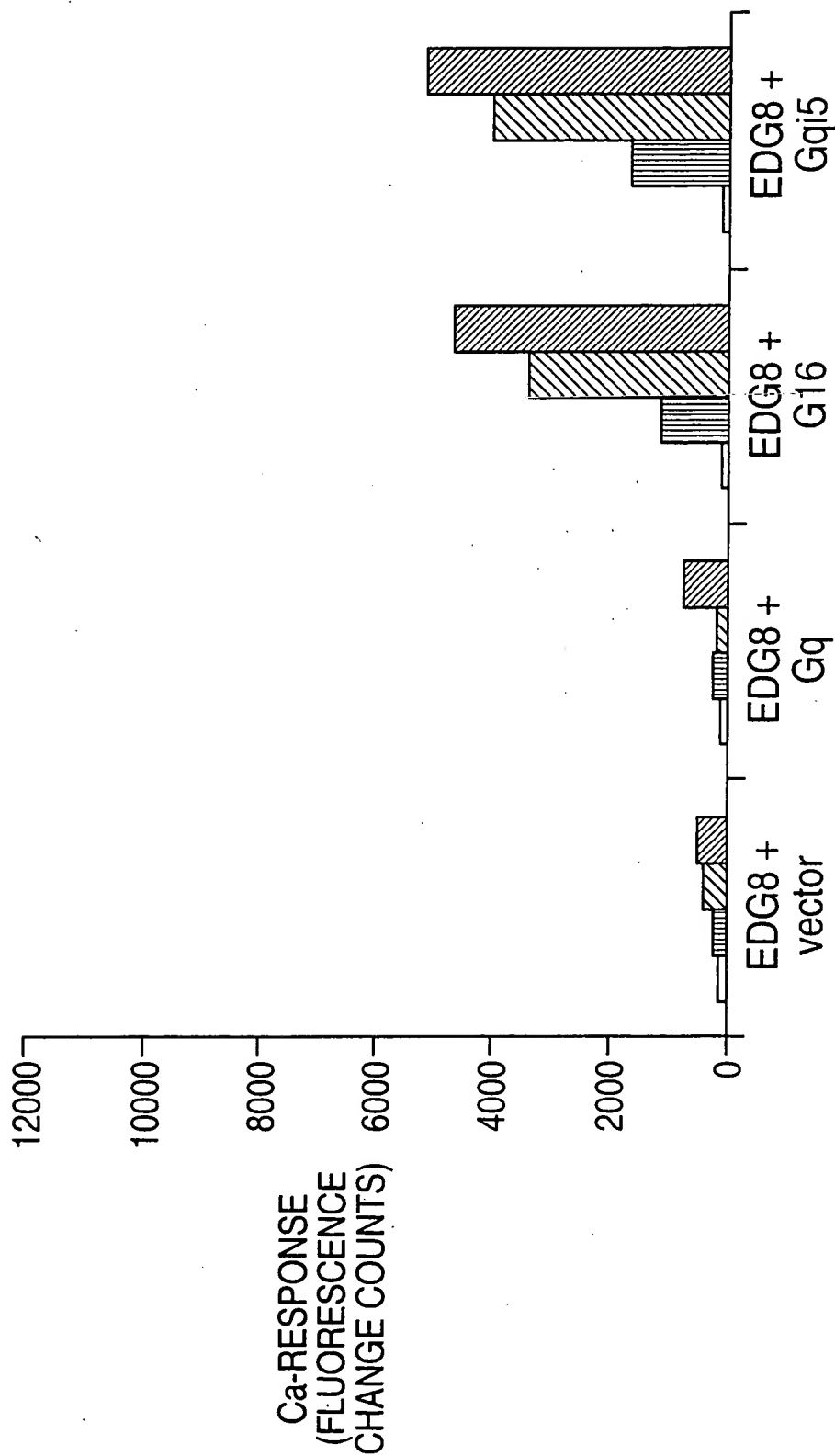


**FIG. 8**



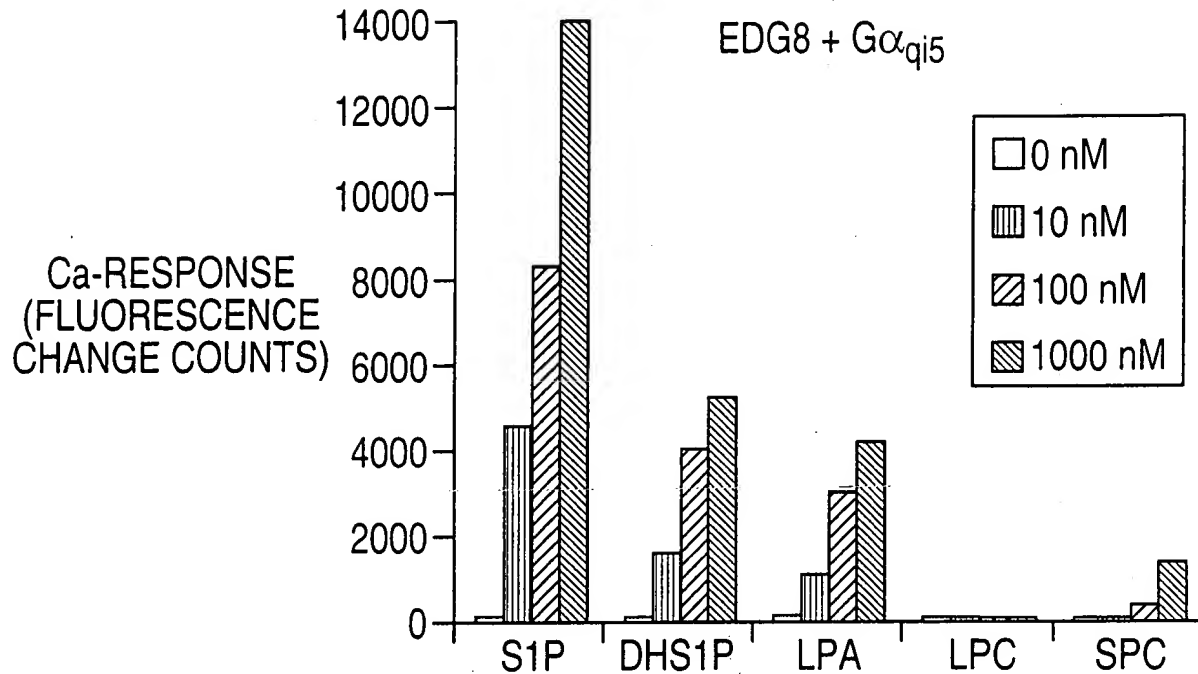


**FIG. 9**

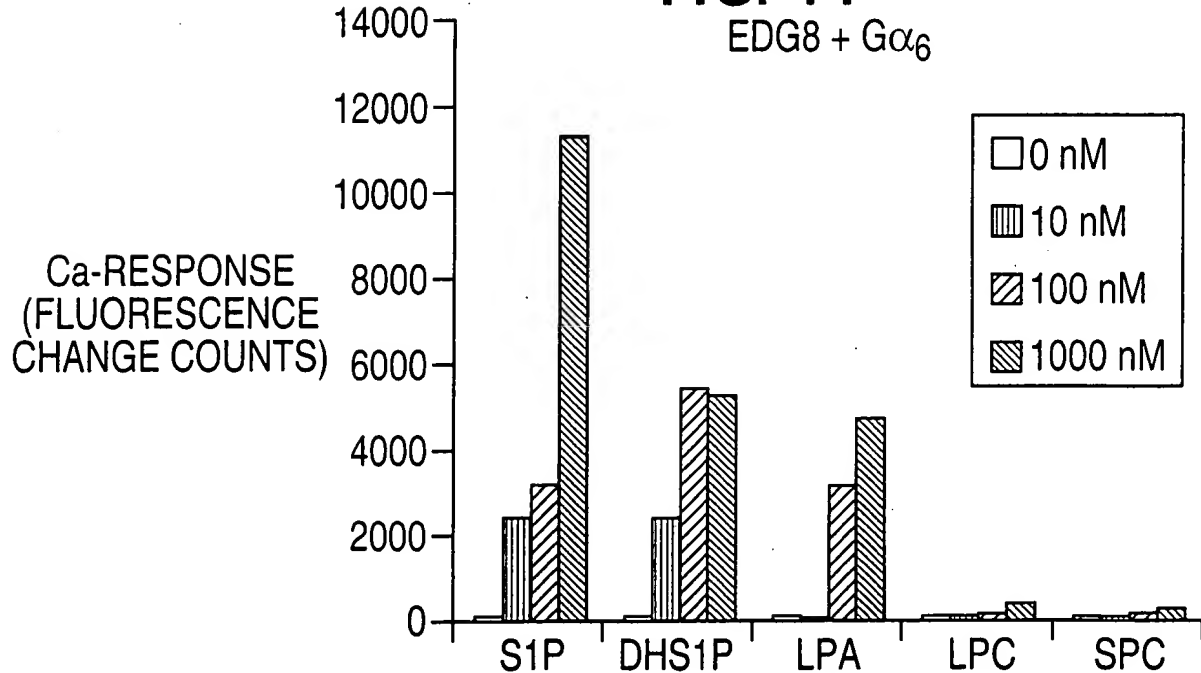




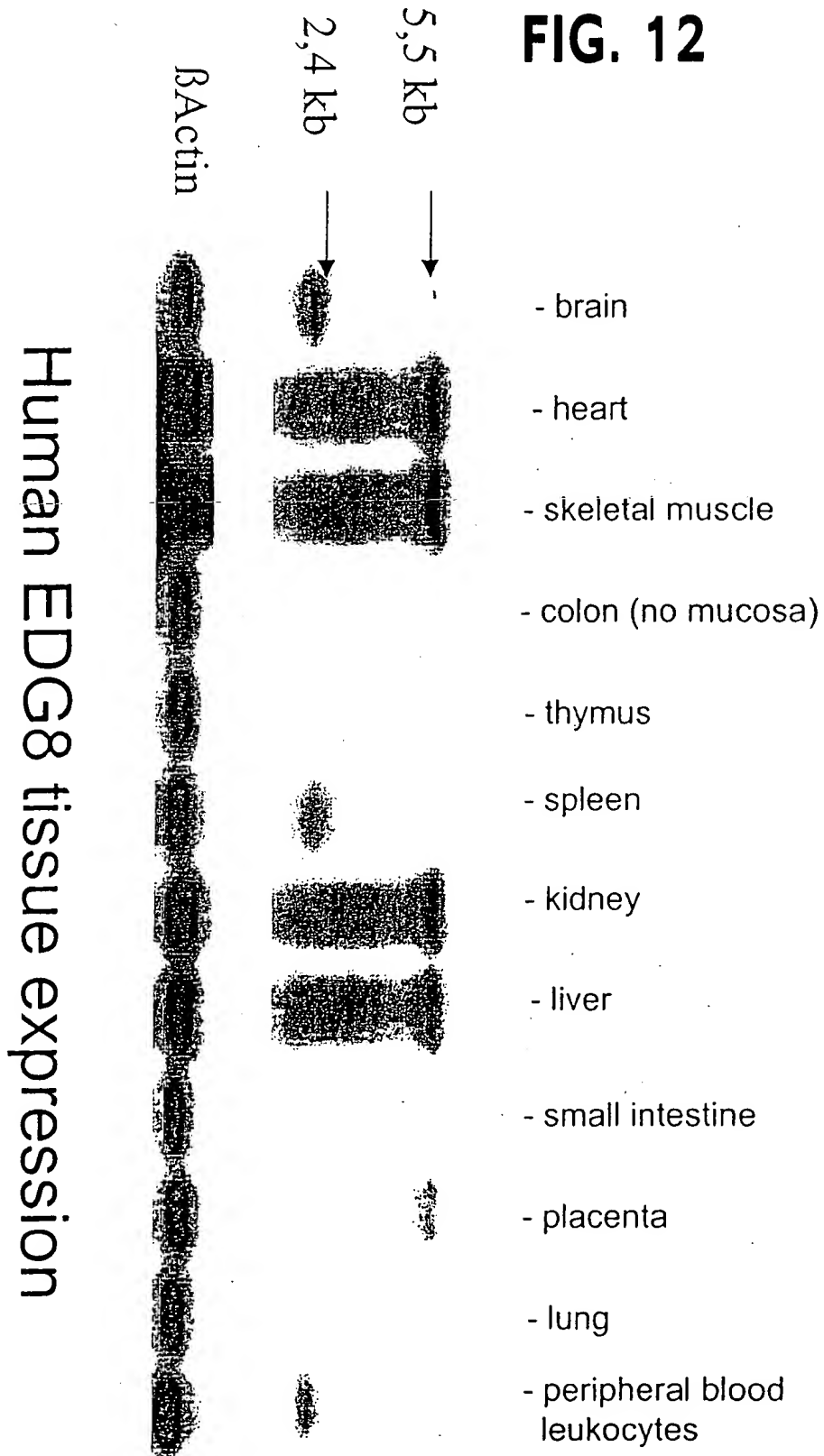
**FIG. 10**



**FIG. 11**



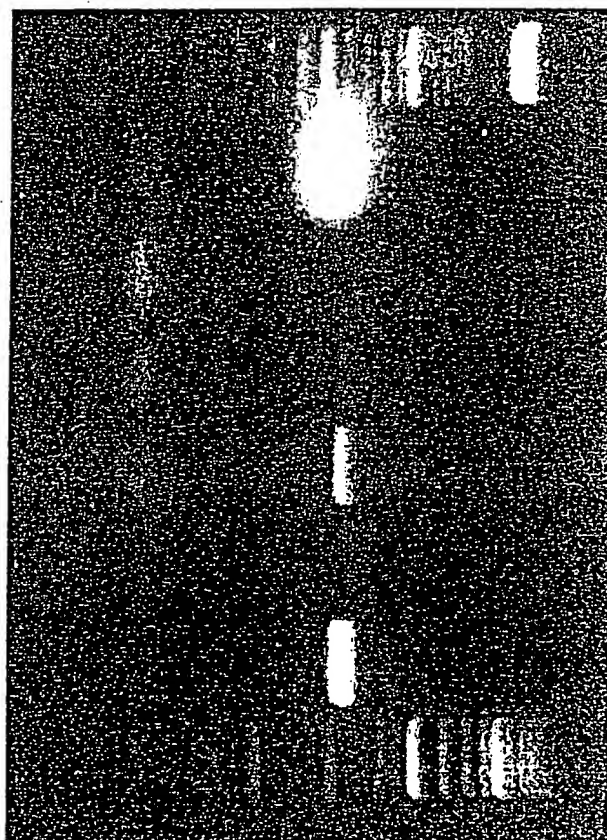
**FIG. 12**



15915 U.S. PTO  
06/02/03

**FIG. 13**

522 bp  
↓

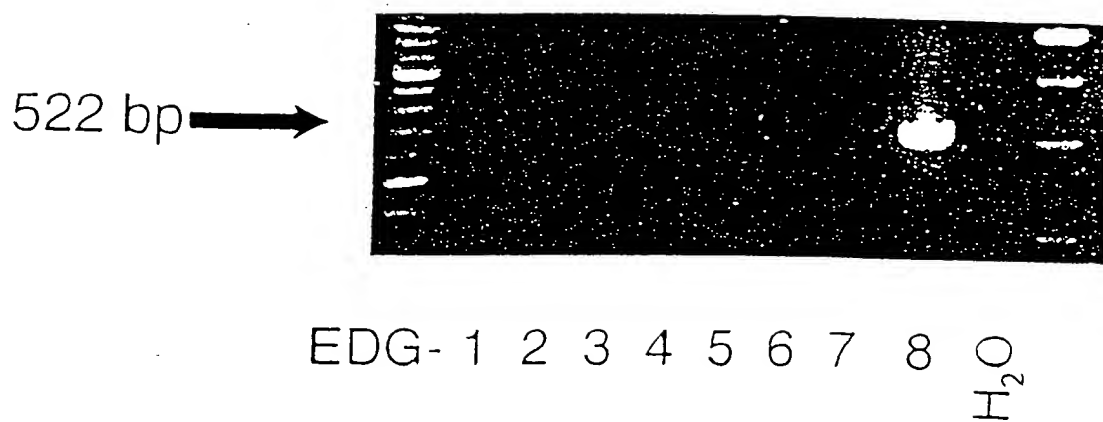


Pos. control  
neg. control  
HUVECS  
HCAEC  
HMVEC-L  
HPAEC

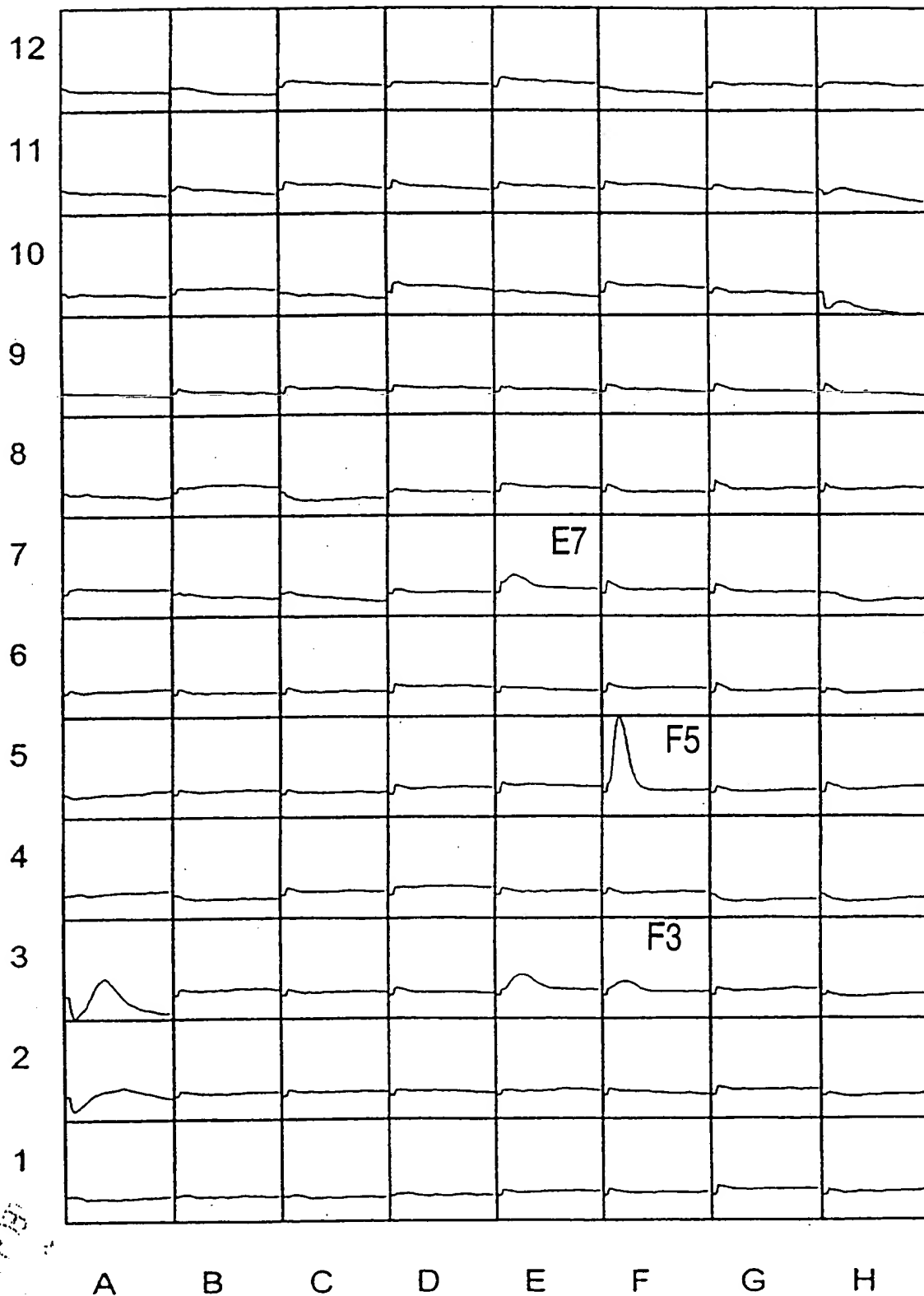
RECEIVED  
JUN 10 2003  
LECH CENTER

15915 U.S. PTO  
06/02/03

**FIG. 14**



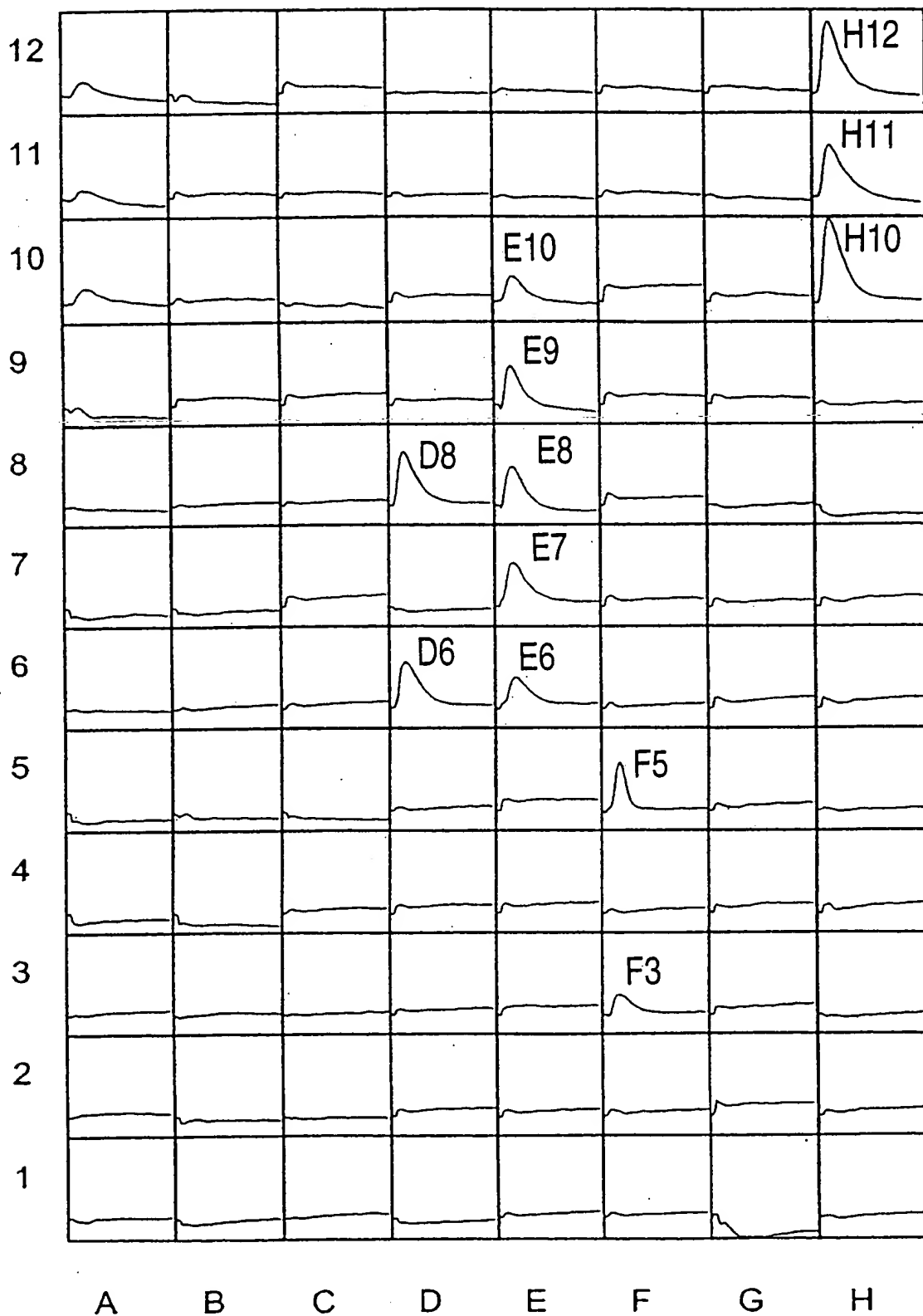
**FIG. 15**  
qi5 background



RECEIVED  
JUN 02 2003  
FBI/DOJ  
FBI/DOJ  
FBI/DOJ



**FIG. 16**  
rEDG8



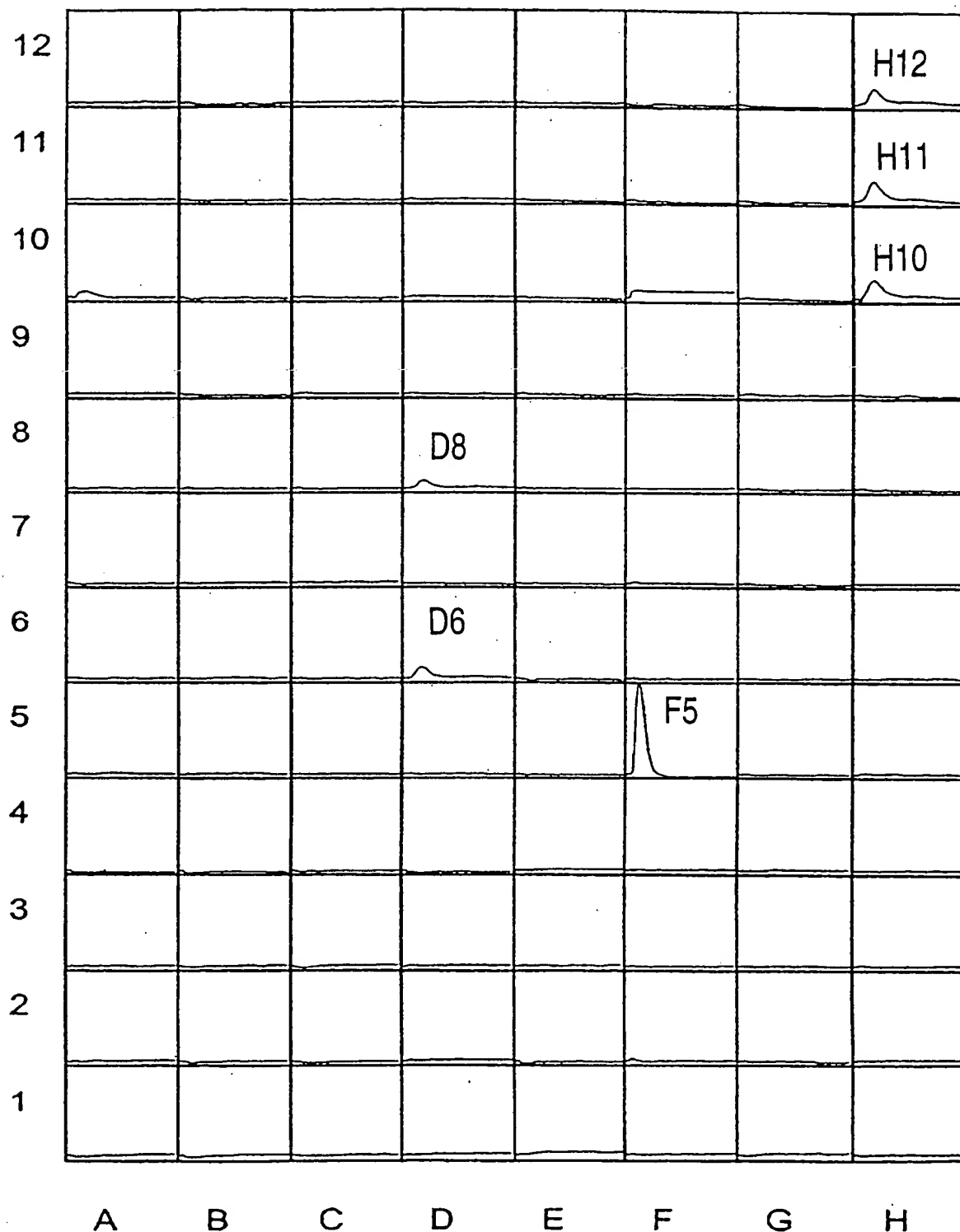


**FIG. 17**  
Fluorescence Change counts

Wells	Lipid	background	rEDG8	stand. response
H10-H12	1 $\mu$ M S1P	0	5196	5196
F5	1 $\mu$ M LPA	5893	4327	-1566
F3	1 $\mu$ M cPAF	1017	1570	553
E10	1 $\mu$ M EPA PAF	0	1354	1354
E9	1 $\mu$ M AA PAF	0	3121	3121
E8	1 $\mu$ M Enantio PAF	0	3883	3883
E7	1 $\mu$ M paf C18:1	1256	3765	2509
E6	1 $\mu$ M Lyso PAF	0	2421	2421
D8	1 $\mu$ M dhS1P	0	5144	5144
D6	1 $\mu$ M S1P	0	3672	3672

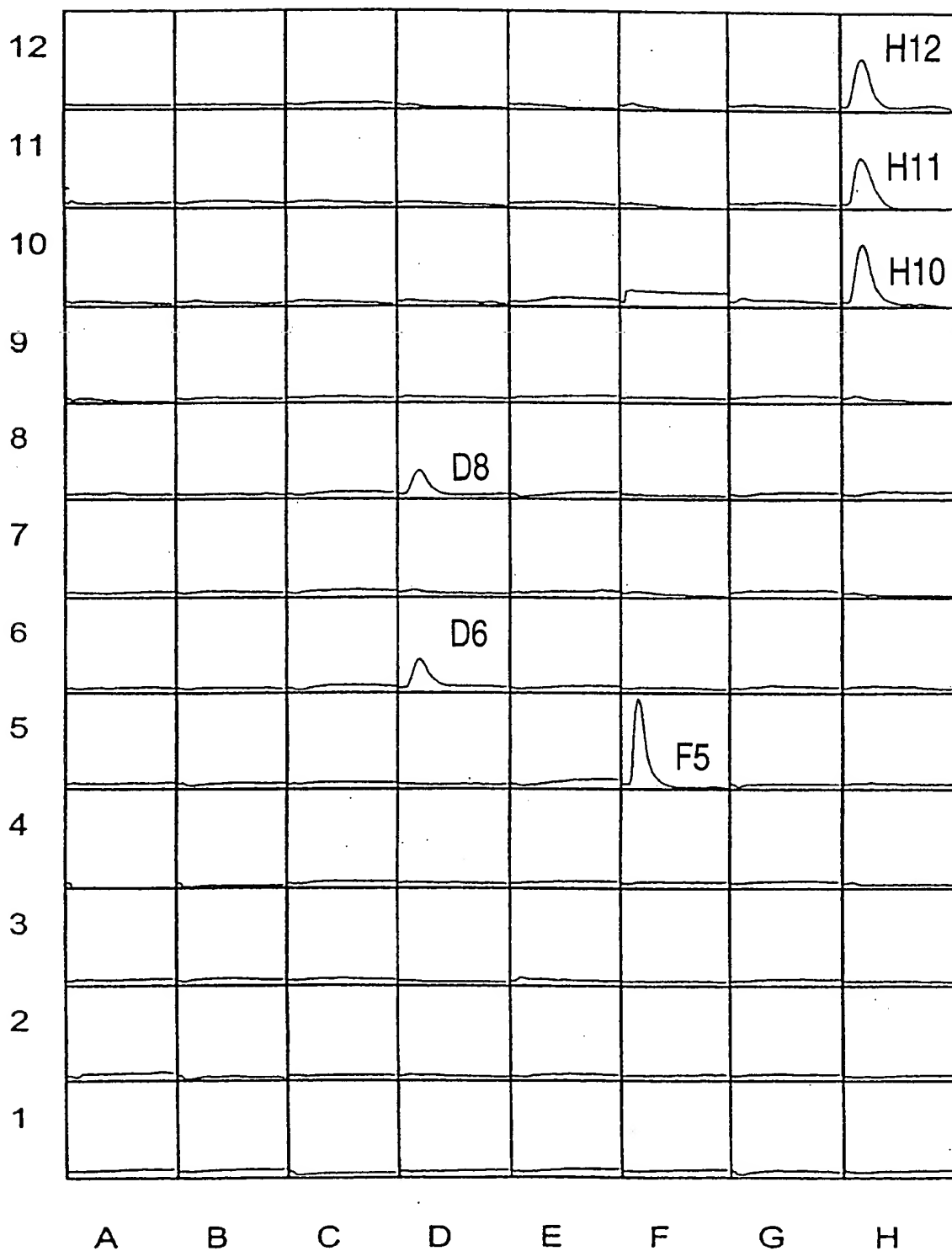


**FIG. 18**  
qi5 background in HEK





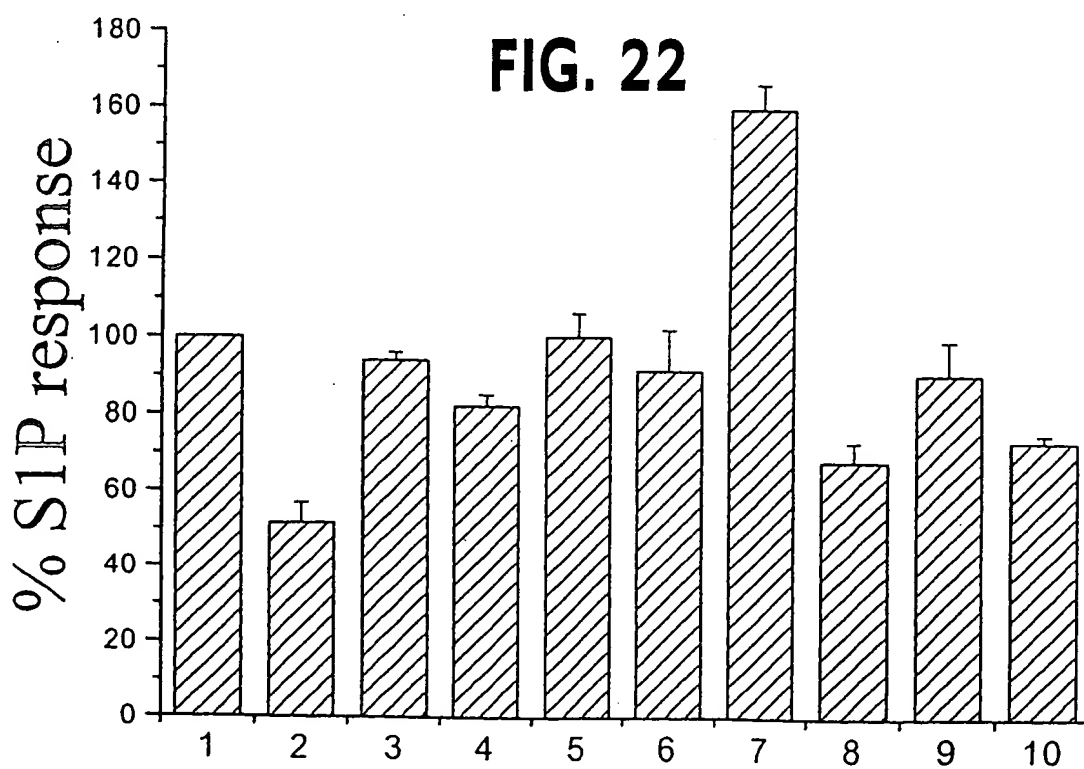
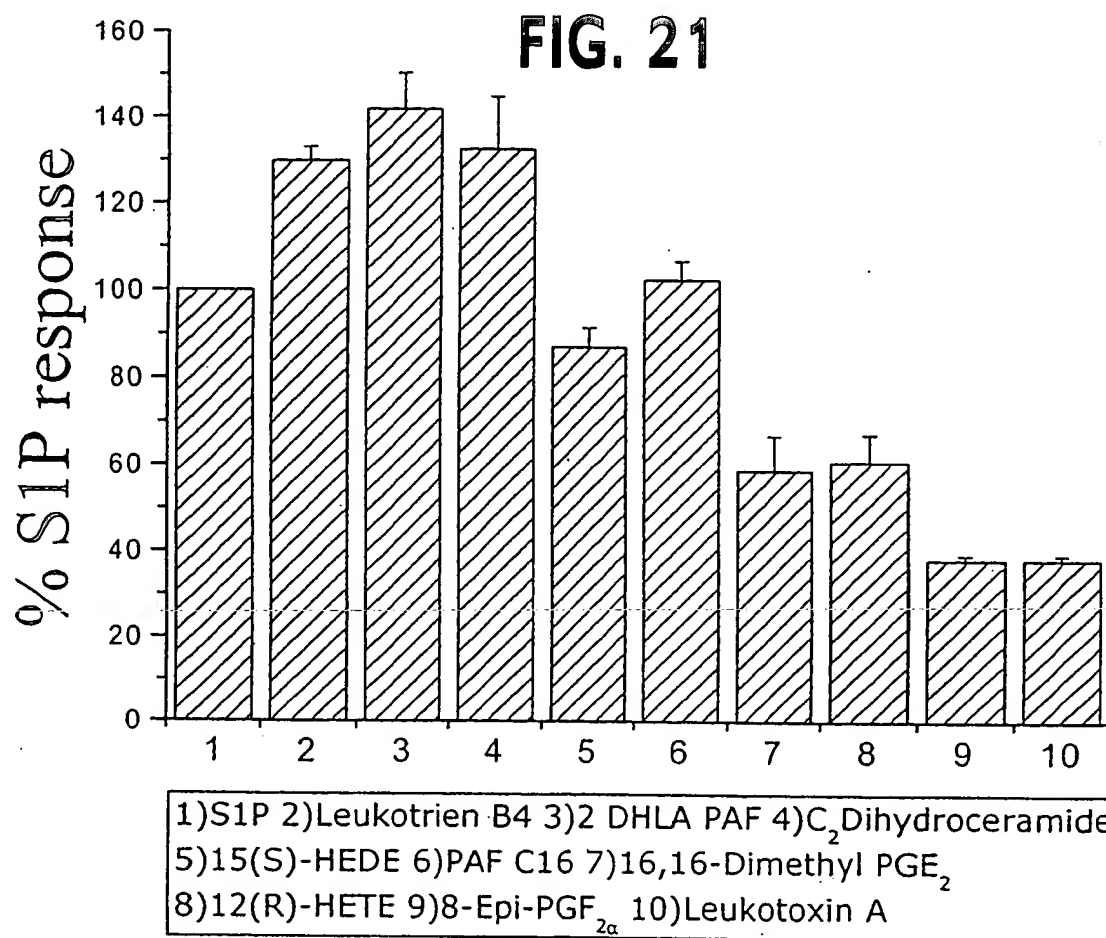
**FIG. 19**  
hEDG8





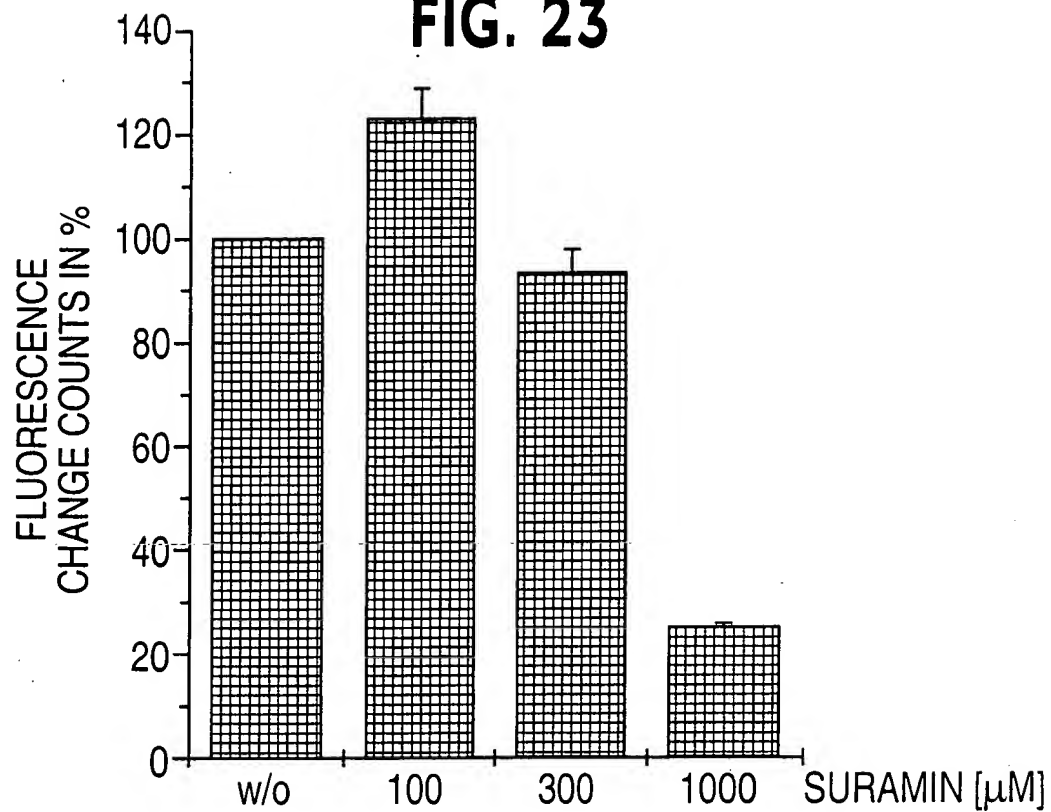
**FIG. 20**  
Fluorescence change counts

Wells	Lipid	background	hEDG8	stand. response
H10-H12	1 $\mu$ M S1P	3696	9493	5797
F5	1 $\mu$ M LPA	18004	16333	-1671
D8	1 $\mu$ M dhS1P	1683	4522	2839
D6	1 $\mu$ M S1P	2273	5605	3332





**FIG. 23**



**FIG. 24**

